

FIGURE 1-1

FIGURE 1-1
FIGURE 1-2
FIGURE 1-3
FIGURE 1-4
FIGURE 1-5

-80 -60 -40 31  
-28 AGTATTGTTGTCGTGTTGCCCTTGTTAGGGCGTCATCCCTCAAGTGATCACTAGTTCAA 31

-20 -1 20  
32 GAGTCCTGGAATCTTTTCACATCCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTC 91  
-8 M N T S H L L A L L L 11

40 60 80  
92 CCAAAATCTCCACAAGGTGAAAACAGAAAGCAACCCCTGGGCAACCCATACAACTTCTCT 151  
12 P K S P Q G E N R S K P L G T P Y N F S 31

100 120 140  
152 GAACATTGCCAGGATTCCGTTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAG 211  
32 E H C Q D S V D V M V F I V T S Y S I E 51

160 180 200  
212 ACTGTCGTGGGGTCCCTGGGTAACCTCTGCCTGATGTGTGACTGTGTGAGGCAGAAGGAG 271  
52 T V V G V L G N L C L M C V T V R Q K E 71

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FIGURE 1-2

272	AAAGCCAACGTGACCAACCTGCTTATCGCCCAACCTGGCCTTCTCTGACTTCCTCATGTGC	220	240	260	331
72	K A N V T N L L I A N L A F S D F L M C				91
332	CTCCTCTGCCAGCCGCTGACCGCGCTACACCATCATGGACTACTGGATCTTTGGAGAG	280	300	320	391
92	L L C Q P L T A V Y T I M D Y W I F G E				111
392	ACCCTCTGCAAGATGTGGGCGCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCG	340	360	380	451
112	T L C K M S A F I Q C M S V T V S I L S				131
452	CTCGTCCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCCAACAGGCTGGAAGCCC	400	420	440	511
132	L V L V A L E R H Q L I I N P T G W K P				151
512	AGCATCTCACAGGCCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCCTGTCTCTCC	460	480	500	571
152	S I S Q A Y L G I V L I W V I A C V L S				171

3/19

FIGURE 1-3

520	540	560	
572 CTGCCCITCCTGGCCACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCT			631
172 L P F L A N S I L E N V F H K N H S K A			191
580	600	620	
632 CTGGAGTTCTGGCAGATAAGGTGGTCTGTACCGAGTCCCTGGCCACTGGGCTCACCCCGC			691
192 L E F L A D K V V C T E S W P L A H H R			211
640	660	680	
692 ACCATCTACACACCTTCCTGCTCCTCTTCCAGTACTGCCCTCCCACTGGGCTTCATCCTG			751
212 T I Y T T F L L L F Q Y C L P L G F I L			231
700	720	740	
752 GTCTGTATGCACGCATCTACCGCGCCTGCAGAGGCAGGGCGCGTGTTCACAAGGC			811
232 V C Y A R I Y R R L Q R Q G R V F H K G			251
760	780	800	
812 ACCTACAGCTTGGAGCTGGGCACATGAAGCAGGTCAATGTGGTGGTGATGGTG			871
252 T Y S L R A G H M K Q V N V V L V V M V			271

4/19

FIGURE 1-4

872	GTGGCCTTTGCCCTGCTCTGGCTGCCTCTGTCATGTGTTCAACAGCCCTGGAAGACTGGCAC	931
272	V A F A V L W L P L H V F N S L E D W H	291
	820 840 860	
932	CATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACCTTGCTTGCC	991
292	H E A I P I C H G N L I F L V C H L L A	311
	880 900 920	
992	ATGGCCTCCACCTGCGTCAACCCATCTCATCTATGGCTTTCTCAACACCACTTCAAGAAG	1051
312	M A S T C V N P F I Y G F L N T N F K K	331
	940 960 980	
1052	GAGATCAAGGCCCTGGTGTGACTTGCCAGCAGAGCGCCCCCTGGAGGAGTCGGAGCAT	1111
332	E I K A L V L T C Q Q S A P L E E S E H	351
	1000 1020 1040	
1112	CTGCCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGTCCCTGAGGCTAAGTGGCAGG	1171
352	L P L S T V H T E V S K G S L R L S G R	371
	1060 1080 1100	

## FIGURE 1-5

5/19

1172	TCCAATCCCATTTTAACCAAGGTCTAGGTCTTCTCCCTGCCATGTCCCTTGCCAGGCTCTTC	1120	1140	1160	1231
372	S N P I *				375
1180		1200		1220	
1232	CACTAGCTAAGTGGGCACACTGCAAGCTGGGGTGGCACCACCAATTCCTGGCTTCTG				1291

FIGURE 2-1  
FIGURE 2-2  
FIGURE 2-3

FIGURE 2-1

1	hp25a	MNTSHLLALL	LPKSPQGENR	SKPLGTPYNF	SEHCQSDVDV	MVFIVTSYSI	50
	human Y1	MN.STLFSQV	ENHSHVSNFS	ERNAQLLAFE	NDDCHLPLAM	IFTLALAYGA	
	rat Y1	MN.STLFSRV	ENYSHVHYNVS	E.NSPFLAFE	NDDCHLPLAV	IFTLALAYGA	
	mouse Y1	MN.STLFSKV	ENHSHIYNAS	E.NSPLLAFE	NDDCHLPLAV	IFTLALAYGA	
51	hp25a	ETVVGVLGNI	CLMCVTVRQK	EKANVTNLI	ANLAFSDFIM	CLLCQPLTAY	100
	human Y1	VIILGVSGNI	ALIIIIILKQ	EMRNVTNILL	VNLSFSDLLV	AIMCLPFFTV	
	rat Y1	VIILGVSGNI	ALIIIIILKQ	EMRNVTNILL	VNLSFSDLLV	AVMCLPFFTV	
	mouse Y1	VIILGVSGNI	ALIIIIILKQ	EMRNVTNILL	VNLSFSDLLV	AVMCLPFFTV	
101	hp25a	YTINDYWIFG	ETLCKMSAFI	QCMSVTVSIL	SLVLVALERH	QLIINPTGWNK	150
	human Y1	YTLMDHNVFG	RAMCKLNPFV	QCVSITVSIF	SLVLI AVERH	QLIINPRGWR	
	rat Y1	YTLMDHNVFG	ETMCKLNPFV	QCVSITVSIF	SLVLI AVERH	QLIINPRGWR	
	mouse Y1	YTLMDHNVFG	ETMCKLNPFV	QCVSITVSIF	SLVLI AVERH	QLIINPRGWR	
151	hp25a	PSISQAYIGI	VLIWVIA CVL	SLPFIANSIE	ENVFHKNHSH	ALEFLADKVV	200
	human Y1	PNNRHAYVGI	AVIHWLAVAS	SLPFLIYQVM	TDEPFQNVVT.	.LDAYKDKYV	
	rat Y1	PNNRHAYIGI	TVIHWLAVAS	SLPFIYQIIL	TDEPFQNVVS.	.LAAFKDKYV	
	mouse Y1	PNNRHAYIGI	TVIHWLAVAS	SLPFIYQIIL	TDEPFQNVVS.	.LAAFKDKYV	

7/19

FIGURE 2-2

hp25a	201	CTESWPLAHH	RTIYTFLL	FOYCLPLGFI	LVQYARIYRR	LQYGRVFFHK	250
human Y1		CFDQFPBDSH	RLSYTNLLIV	LQYFGPLCFI	FICYFKIYIR	LKRRNNMMDK	
rat Y1		CFDKFPBDSH	RLSYTNLLIV	LQYFGPLCFI	FICYFKIYIR	LKRRNNMMDK	
mouse Y1		CFDKFPBDSH	RLSYTNLLIV	LQYFGPLCFI	FICYFKIYIR	LKRRNNMMDK	
			V				
	251	GTYS.LRAGH	MKQNVVLLV	MVAFVAVLML	PLHVFNSLED	WNHQAIPICH	300
hp25a		MRDNKYRSSE	TKRINIMLLS	IVVAFVAVCWL	PLTI FNTVFD	WNHQA IATCN	
human Y1		IRDSKYRSSE	TKRINVMLLS	IVVAFVAVCWL	PLTI FNTVFD	WNHQA IATCN	
rat Y1		IRDSKYRSSE	TKRINIMLLS	IVVAFVAVCWL	PLTI FNTVFD	WNHQA IATCN	
mouse Y1			VI				
	301	GNLITLVCHL	LAMASTCVNP	FVYGPLNTNF	KKEIKALVLT	CQQSAPLEES	350
hp25a		HNLLFLLC	TAMISTCVNP	IFYGFLNKNF	QRDLQOFFNF	CDFRSRDDDY	
human Y1		HNLLFLLC	TAMISTCVNP	IFYGFLNKNF	QRDLQOFFNF	CDFRSRDDDY	
rat Y1		HNLLFLLC	TAMISTCVNP	IFYGFLNKNF	QRDLQOFFNF	CDFRSRDDDY	
mouse Y1		HNLLFLLC	TAMISTCVNP	IFYGFLNKNF	QRDLQOFFNF	CDFRSRDDDY	
			VII				

8/19

FIGURE 2-3

hp25a	351	388
human Y1	PHLPSTVHT EVSKGSRRLS GRSNPI*....	.....
rat Y1	ETIAMSTMHT DVSKTSLKQA SPVAFKKINN	NDDNEKI*
mouse Y1	ETIAMSTMHT DVSKTSLKQA SPVAFKKISM	N.DNEKI*
	ETIAMSTMHT DVSKTSLKQA SPVAFKKISM	N.DNEKV*



9/19

## FIGURE 3-1

FIGURE 3-1
FIGURE 3-2
FIGURE 3-3
FIGURE 3-4

-170

-150

-130

ATAGCTCTCAAGCCATAAGATATAAGTAGCTAAGAATTGTCTCCCTCTCCCTGTCCCTTG

-110

-90

-70

TTCTTACCTGGTTCCATTTTACATGCCTGGACCTTTGAGTTCCATTTGTTTGTTCAG

-50

-30

-10

GCTACACTCAGAAGTGGGCCCTTTAGTCTTGAAGTTCCTGGTCTTCTCACACCCACCATG

M

10

30

50

AATACCTCTCATCTCATGGCCTCCCTTTCTCCGGCATTCTTACAAGGTAAGAATGGGACC

N T S H L M A S L S P A F L Q G K N G T

70

90

110

AACCCACTGGATTCCCTCTATAATCTCTCTGACGGCTGCCAGGATTCGGCAGATCTGTTG

N P L D S L Y N L S D G C Q D S A D L L

130

150

170

GCCTTCATCATCACCACCTACAGCGTTGAGACCGTCTTGGGGGTCCTAGGAAACCTCTGC

A F I I T T Y S V E T V L G V L G N L C

190

210

230

TTGATATTTGTGACCACAAGGCAAAAGGAAAAGTCCAATGTGACCAACCTACTCATTGCC

L I F V T T R Q K E K S N V T N L L I A

10/19

FIGURE 3-2

250 270 290  
AACCTGGCCTTCTCTGACTTCCTCATGTGTCTCATCTGCCAGCCGCTCACGGTCACCTAC  
N L A F S D F L M C L I C Q P L T V T Y

310 330 350  
ACCATCATGGACTACTGGATCTTCGGCGAAGTCCTTTGCAAGATGTTAACGTTTCATCCAG  
T I M D Y W I F G E V L C K M L T F I Q

370 390 410  
TGTATGTCGGTGACAGTCTCCATCCTCTCACTGGTCCTTGTGGCCCTGGAGAGGCACCAG  
C M S V T V S I L S L V L V A L E R H Q

430 450 470  
CTCATTATCAACCCGACTGGCTGGAAACCCAGCATTTCCTCAGGCCTACCTGGGGATTGTG  
L I I N P T G W K P S I S Q A Y L G I V

490 510 530  
GTCATCTGGTTCATTTCTTGTTTCCTCTCCTTGCCCTTCCTGGCCAATAGCATCCTGAAC  
V I W F I S C F L S L P F L A N S I L N

550 570 590  
GACCTCTTCCACTACAACCACTCTAAGGTTGTGGAGTTTCTGGAAGACAAGGTTGTCTGC  
D L F H Y N H S K V V E F L E D K V V C

610 630 650  
TTTGTGTCCTGGTCCTCGGATCACCACCGCCTCATCTACACCACCTTTCTGCTGCTCTTC  
F V S W S S D H H R L I Y T T F L L L F

11/19

FIGURE 3-3

670                      690                      710  
 CAATACTGCGTCCCTCTGGCCTTCATCCTGGTCTGCTACATGCGTATCTATCAGCGCCTG  
 Q Y C V P L A F I L V C Y M R I Y Q R L

730                      750                      770  
 CAGAGGCAGAGGCGTGCGTTCCACACGCACACTTGCAGCTCACGAGTGGGGCAGATGAAG  
 Q R Q R R A F H T H T C S S R V G Q M K

790                      810                      830  
 CGGATCAATGGCATGCTCATGGCAATGGTGACTGCCTTTGCAGTTCTCTGGCTGCCCCTG  
 R I N G M L M A M V T A F A V L W L P L

850                      870                      890  
 CATGTGTTCAACACTCTGGAGGACTGGTACCAGGAAGCCATCCCTGCTTGCCATGGCAAC  
 H V F N T L E D W Y Q E A I P A C H G N

910                      930                      950  
 CTCATCTTCTTGATGTGCCACCTGTTTGCCATGGCTTCCACCTGTGTCAACCCTTTCATC  
 L I F L M C H L F A M A S T C V N P F I

970                      990                      1010  
 TATGGCTTTCTCAACATCAACTTCAAGAAGGACATCAAGGCTCTGGTTCTGACCTGCCGT  
 Y G F L N I N F K K D I K A L V L T C R

1030                      1050                      1070  
 TGCAGGCCACCTCAAGGGGAGCCTGAGCCTCTGCCCCTGTCCACTGTGCACACGGACCTC  
 C R P P Q G E P E P L P L S T V H T D L

12/19

## FIGURE 3-4

1090 1110 1130  
TCCAAGGGATCTATGAGGATGGGTAGCAAGTCTAACGTCATGTAGTCATGTCTAGGCTCT  
S K G S M R M G S K S N V M \*

1150 1170 1190  
TCCGCCATTTTCTTTGACACACCCTTTCACTGAGCTAAGTAGACACAATGCAAGCTGTG

1210 1230 1250  
GTATCATCCTGCCATTTCTGGTCTTTGGGGCCAGACAGGCGGCAAGAGACTTGAAGCTT

46EYFO'S69564B0

13/19

## FIGURE 4

1 50

Y4rat MNTSHLMASL SPAFLQKNG TNPLDSLNL SDGCQDSADL LAFIITTSV  
Y4hum MNTSHLLALL LPKSPQGENR SKPLGTPYNF SEHCQDSVDV MVFIVTSYSI

51 100

— I — II —

Y4rat ETVLGVLGNL CLIFVTTRQK EKSNTNLLI ANLAFSDFLM CLICQPLTVT  
Y4hum ETVVGVLGNL CLMCVTVRQK EKANVTNLLI ANLAFSDFLM CLICQPLTAV

101 150

— III —

Y4rat YTIMDYWIFG EVLCRMLTFI QCMSVTVSIL SLVLVALERH QLIINPTGWK  
Y4hum YTIMDYWIFG ETLCKMSAFI QCMSVTVSIL SLVLVALERH QLIINPTGWK

151 200

— IV —

Y4rat PSISQAYLGI VVINFISCFL SLPFLANSIL NDLFHYNHSK VVEFLEDKVV  
Y4hum PSISQAYLGI VLIWVIACVL SLPFLANSIL ENVFHKNHSK ALEFLADKVV

201 250

— V —

Y4rat CFVSNSSDHH RLIYTTFLLL PQYCVPLAFI LVCYMRIYQR LQRORRAFHT  
Y4hum CTESWPLAHH RTIYTTFLLL PQYCLPLGFI LVCYARIYRR LQRQGRVPHK

251 300

— VI —

Y4rat HTCSSRVGQM KRINGMLMAN VTAPAVLNLP LHVNTLEDW YQRAIPACHG  
Y4hum GTYSLRAGHM KQVNVVLVVM VVAPAVLNLP LHVNSLEDW HHEAIPICHG

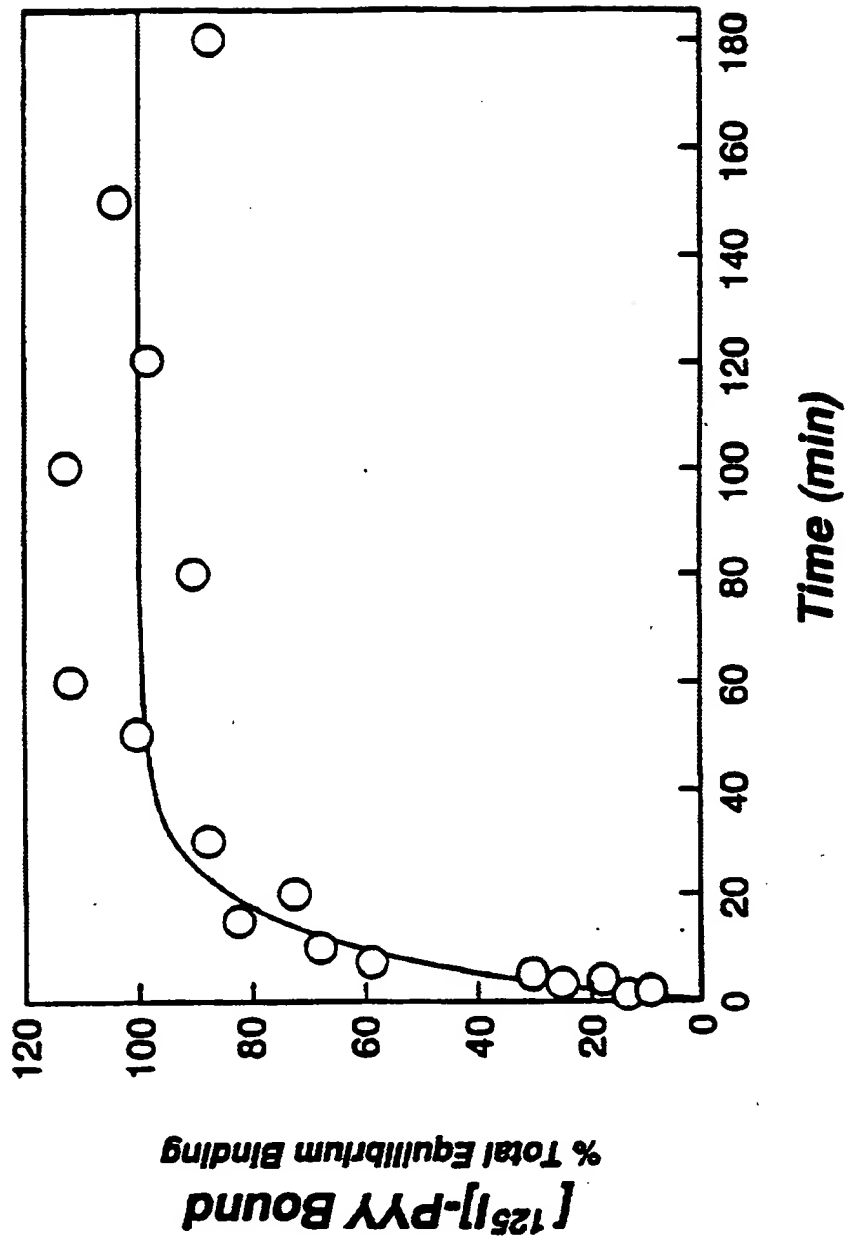
301 350

— VII —

Y4rat NLIFLMCHLF AMASTCVNPF IYGFLNINFK KDIKALVLTG RCRPPQGEPE  
Y4hum NLIFLVCHLL AMASTCVNPF IYGFLNTNFK KBIKALVLTG QQSAPLEESE

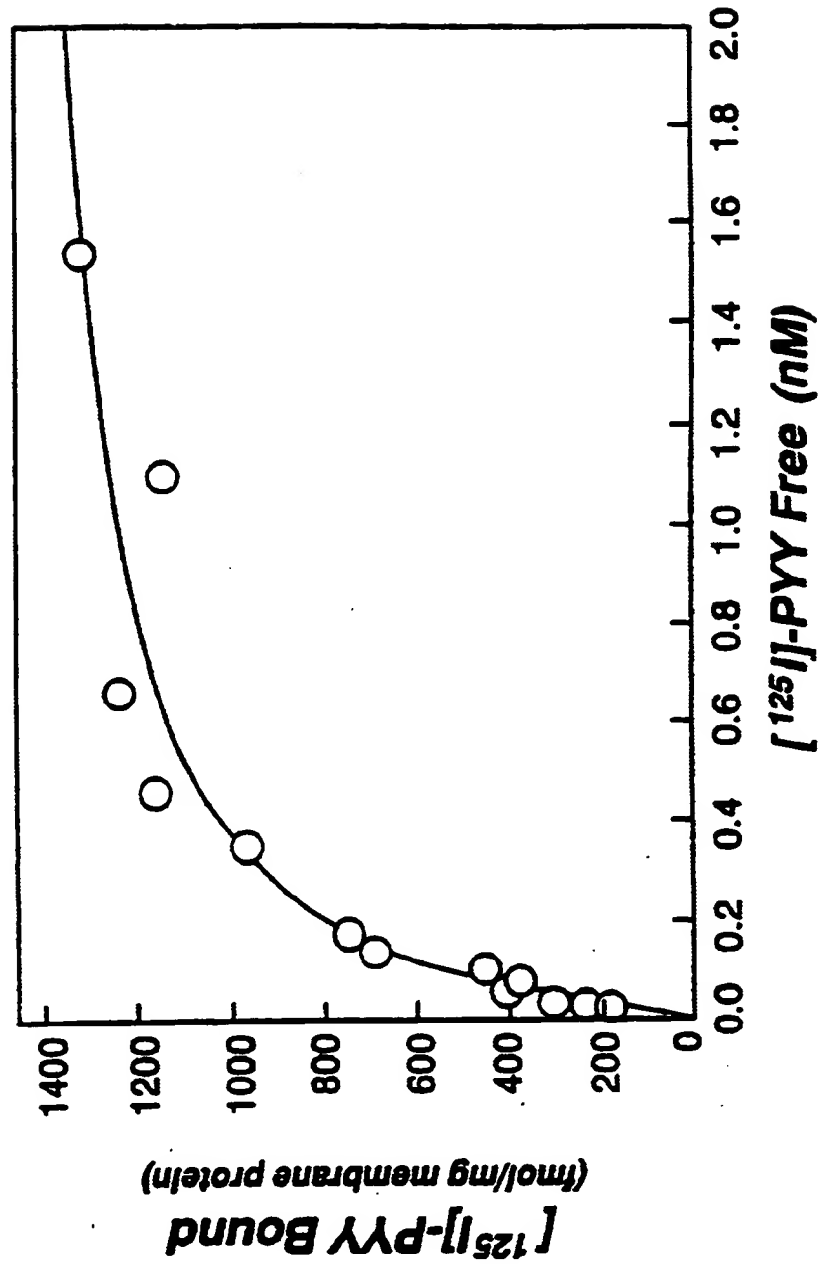
25E110\* 35956480

FIGURE 5



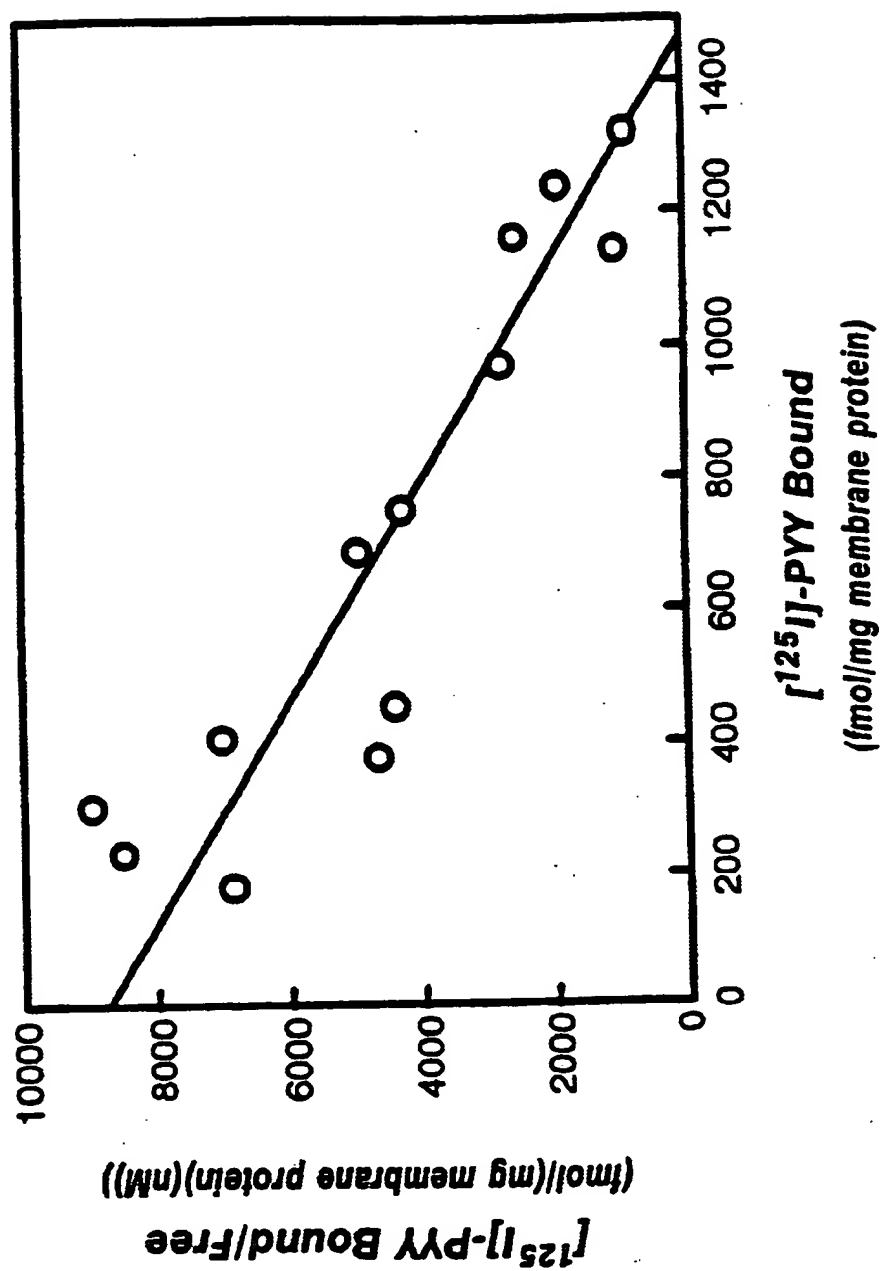
15/19

FIGURE 6A



16/19

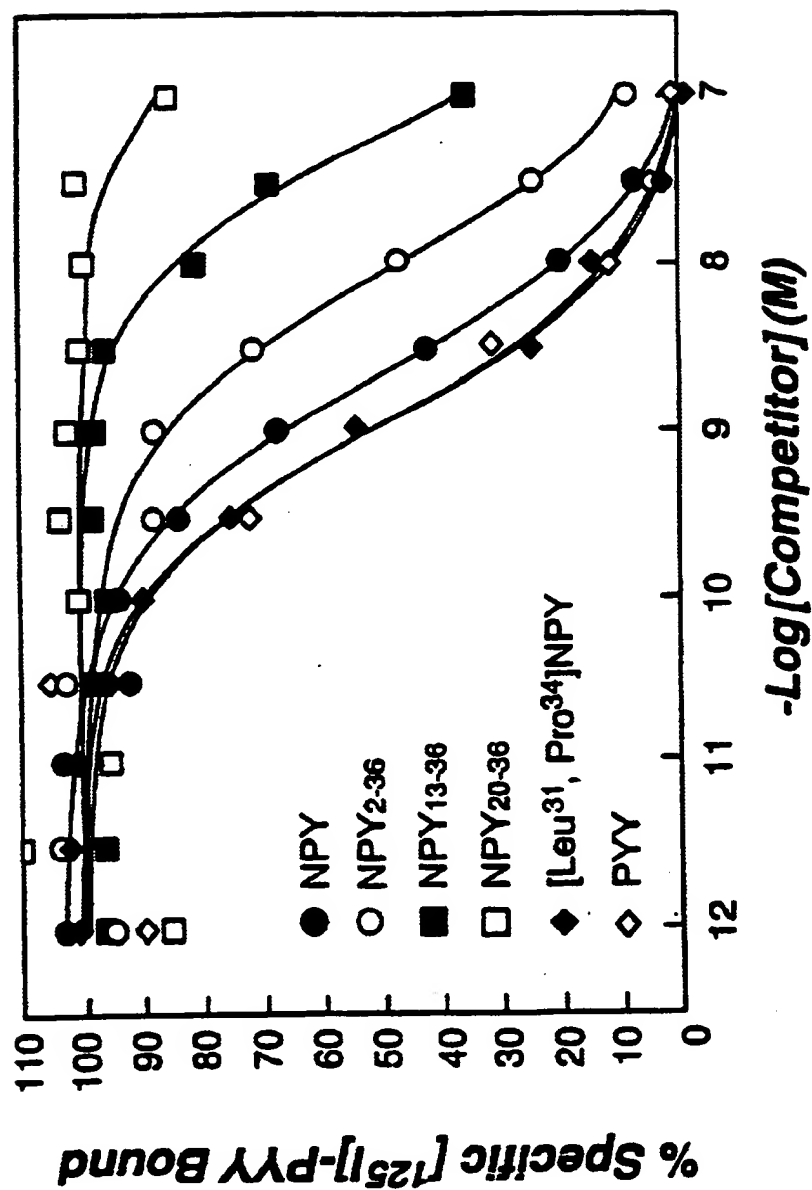
FIGURE 6B





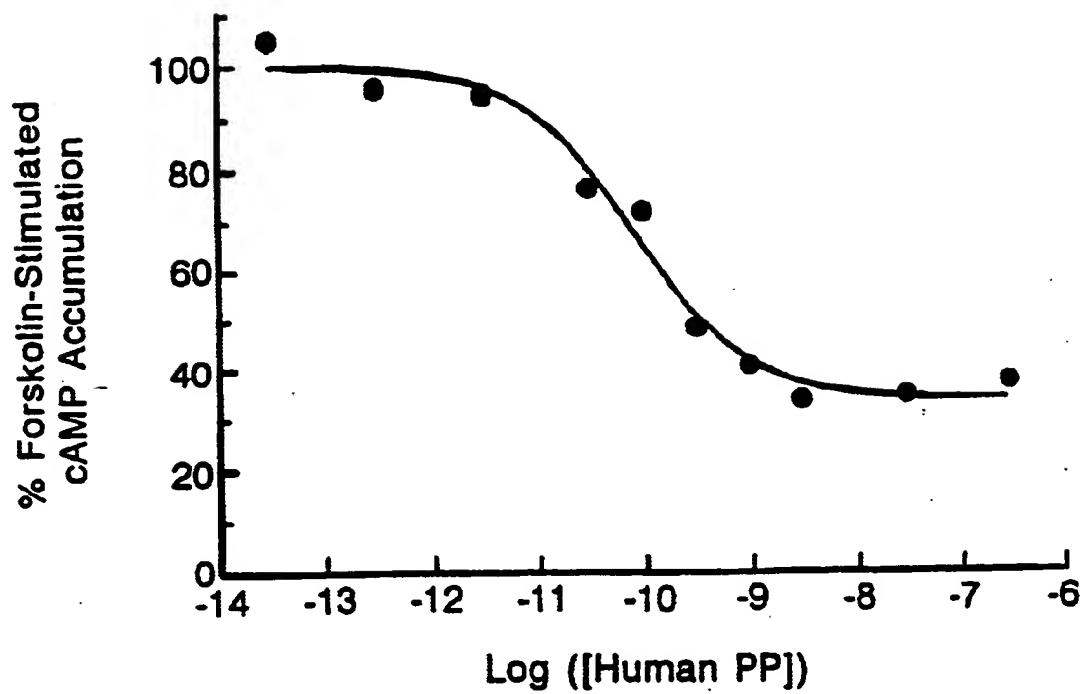
17/19

FIGURE 7

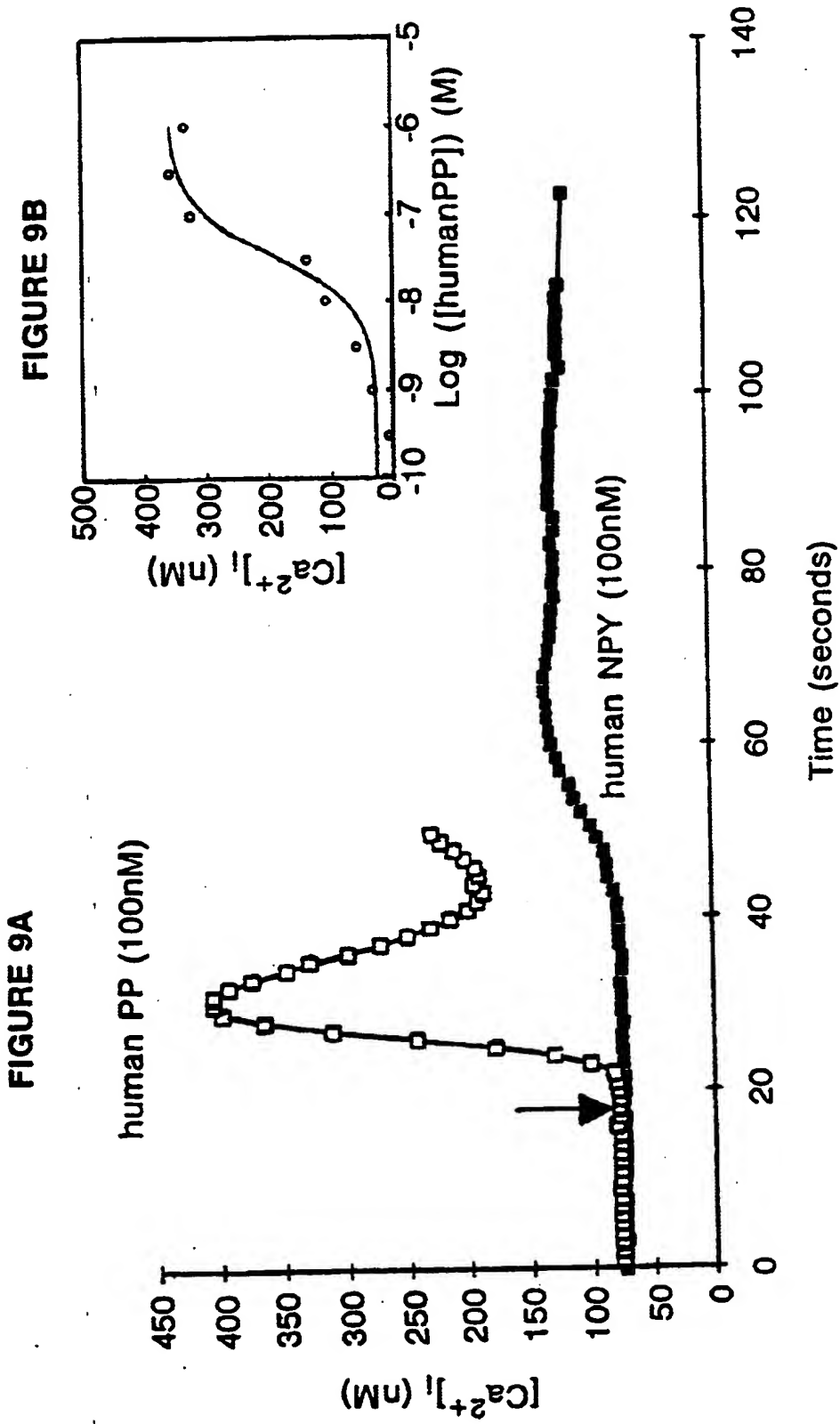


18/19

FIGURE 8



19/19



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